

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 20:03:53 ; Search time 113 Seconds
(without alignments)
7180.809 Million cell updates/sec

Title: US-09-456-306-1

Perfect score: 2160
Sequence: 1 tttagggcgatctctgtgag.....gggtcccatgagatgcct 2160

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_36:*

1: /cgn2_2/gcgdata/geneseq/geneseq/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseq/NA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseq/NA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseq/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseq/NA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseq/NA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseq/NA1986.DAT:*
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9: /cgn2_2/gcgdata/geneseq/geneseq/NA1988.DAT:*
10: /cgn2_2/gcgdata/geneseq/geneseq/NA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseq/NA1990.DAT:*
12: /cgn2_2/gcgdata/geneseq/geneseq/NA1991.DAT:*
13: /cgn2_2/gcgdata/geneseq/geneseq/NA1992.DAT:*
14: /cgn2_2/gcgdata/geneseq/geneseq/NA1993.DAT:*
15: /cgn2_2/gcgdata/geneseq/geneseq/NA1994.DAT:*
16: /cgn2_2/gcgdata/geneseq/geneseq/NA1995.DAT:*
17: /cgn2_2/gcgdata/geneseq/geneseq/NA1996.DAT:*
18: /cgn2_2/gcgdata/geneseq/geneseq/NA1997.DAT:*
19: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT:*
20: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131.6	6.1	7900	18	Staphylococcus aure
2	87.2	4.0	260	21	E.coli promoter re
3	72.6	3.4	1713	11	Pyruvate oxidase (
4	72.6	3.4	1713	11	Pyruvate oxidase (
5	60.8	2.8	2841	17	E. coli livGMEDA O
6	60.8	2.8	2841	17	E. coli thirABC Ope
7	60.8	2.8	2841	17	Escherichia coli 1
8	59.8	2.8	1928	16	Streptococcus pneu
9	59.8	2.8	25002	19	Streptococcus pneu
10	58.2	2.7	2280	19	S. pneumoniae deli
11	56.8	2.6	2702	19	Plant acetoalactate
12	55.2	2.6	2520	9	C3 mutant gene enc

13	55.2	2.6	2520	12	011495
14	55.2	2.6	2520	13	028388
15	55.2	2.6	2520	16	081182
16	55.2	2.6	2520	17	T33353
17	55.2	2.6	2520	18	T72862
18	55.2	2.6	2930	12	011494
19	55.2	2.6	2930	13	028387
20	55.2	2.6	2930	16	081181
21	55.2	2.6	2930	18	T72863
22	55.2	2.6	2946	9	N81458
23	55.2	2.6	2946	17	T33352
24	51.2	2.4	3146	9	N81713
25	50.6	2.3	3230	9	N96290
26	50.6	2.3	6211	19	V52141
27	50	2.3	1776	9	N81031
28	49.6	2.3	2523	13	026001
29	49.4	2.3	2365	19	V11890
30	49.4	2.3	2365	19	V11891
31	49.4	2.3	2907	12	011496
32	49.4	2.3	2907	13	028389
33	49.4	2.3	2907	16	081183
34	49.4	2.3	2907	18	T72864
35	48.2	2.2	1969	14	034553
36	48.2	2.2	1969	14	034551
37	48.2	2.2	1969	14	034552
38	48.2	2.2	1969	19	V24025
39	48.2	2.2	1969	19	V24026
40	48.2	2.2	1969	19	V24027
41	48.2	2.2	2141	13	025382
42	47.6	2.2	2156	18	T77305
43	47.6	2.2	2156	18	T77306
44	47	2.2	1882	16	090522
45	47	2.2	1882	18	T75517

ALIGNMENTS

RESULT 1	
V74449	16-MAR-1999 (first entry)
ID V74449	standard: DNA: 7900 BP.
AC V74449	
XX	
DE	Staphylococcus aureus contig SEQ ID #138.
XX	
KW	Computer readable medium; vaccine; S.aureus infection; Immunodetection;
KW	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW	skin infection; surgical wound infection; scalded skin syndrome;
KW	toxic shock syndrome; ds.
XX	
OS	Staphylococcus aureus.
XX	
FH	Key
FT	misc_feature
FT	541..600
FT	/tag-a
FT	/note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
FT	misc_feature
FT	2341..2400
FT	/tag-b
FT	/note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
FT	misc_feature
FT	4141..4200
FT	/tag-c
FT	/note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

[illegible]

QY	520	agctgacgatactgctgcgtctcttgctgctctggaacacaccccgatcaaggctctt	579
Db	1769	aaatcgtgtgcatctaaagtaactgctggtccctggtttaactatcttaaatgtaagt	1820
QY	580	atgattcgatcgaatgctgctggaaggctgttggccatcgctaaacatatccgaagctcc	639
Db	1829	atgagcccaaaatgataatgtaactgacgaatatatattctgacaaacgaatagtacag	1888
QY	640	agattggttcgaagcttcttcacgaacacgcatcccgagatttgtttaagaaatgctcg	699
Db	1889	cacttgcgaacgaagcatcttccgaagaacaaatttacaanaattatgtgaagtgtacgg	1946
QY	700	gttactgcgaaatggtgaaatggtgtgaagcgtgaacgcatttggatccgcgattc	759
Db	1949	tttaataacacaaattgaaanaagtgacaatgtgtttaaactcgtttaacgaagcaatcc	2008
QY	760	agtcacccatgcgcgtgaaaggtgtgcggtgtgtgaatccctgtgtgatccgtaag	819
Db	2009	gtacggcctatgaaacaaaaggtgtgctgttatttgccttaacgacttaataactg	2066
QY	820	aagacgcagtgtagcgttactatctcaattccatacttcttcgtgcacccctgtgtgt	879
Db	2069	aaaa---aattaaagatacaacgataaacagtagatcatcatgaagacacagtagtat	2122
QY	880	tcccgatccctacgaaagctgcgcagcgtgtgtgaagcgttaacaaacgctaaagctgt	939
Db	2126	caccaaaataataaagacatcaaaaaaagcgtgttaactaatataaagaataaagacgtg	2185
QY	940	cttgttctgcgtgcgcggtgtgaagaatctccgcgcgaaggtgtgtgaagttgtgcgga	999
Db	2186	tcatgttaattggtgtgtagtggtgcgaacaaatgcgaagaatgaagcttaagtgaaatttgaa	2245
QY	1000	agatataatcaacgatacgggcgtgcgtgtgtgtgaagatcaatccacgcgtgaagaatc	1059
Db	2246	tggtcaaaatccgttcattcatcattcaacgactaaacaacatcttgcggatgtcatc	2305
QY	1060	cgtttgaggtgcggaatgctgcgcgtctgtgtgaagcgcctgcgtgtgatagtcccaatg	1119
Db	2306	catatagatcatgttaactttagtgaataatcgtaacnnnnnnnnnnnnnnnnnnnnnnnn	2365
QY	1120	agcgagatcgtctatctatctgtgaacgattctccctatctctgattctccctctaag	1179
Db	2366	nn	2425
QY	1180	acaaagcttgcccaagtgagatatacaacggtgcgacatgtgtgcagctaacgcgtgaagt	1239
Db	2426	aaaatattaaagccatccaattgaca-----caatccataaataatgcgacatgctt	2479
QY	1240	atccggtgacccggtgagtgtgtgcgcacaacatcgaataattttgcctcatgtgaagaaa	1299
Db	2480	tcaatataatgtgaagatgtgtgtgcgatagtanaaatgtgtgttgcatacgtttaactgaaa	2539
QY	1300	aaaaagatcgttccctccttgatccgatact---caagcacacgacgcgtaagtgtgagct	1356
Db	2540	atatataacatgltgcctgaaagaccattcttaacacaaacgtttagaacgtlaaagcgtgtt	2599
QY	1357	cggtgtgtagagacgtiacacacaaagctgcgaagaatgttgcttatccacttgatacag	1416
Db	2600	gggataaatgtagtgaacacaagataaanaataatagtaaacacttaagctccagaagat	2659
QY	1417	ttgcctctattttgaaagagcctgcgcgataaagatgvcggtgtttactgtgataccgca	1476
Db	2660	taatgtgatacaataaataatttataaagatgatagtgtgtgtttcgaagatgtagtga	2719
QY	1477	tgtgtcaatgtgtgcgcatgcgaagtatactcgagaatccgaggaagcgcgcgaacttggg	1536
Db	2720	cagcaacaagtttgcataactcgatactt---aaactgtgttaataacaagttcacca	2776
QY	1537	gttcatctccgcacgcgacgataatgtgtcaatgtcgttgcctcatcgattgtgtgcgaagt	1596
Db	2777	tttcaagtgttgtagtaacaatgtgtgtgcgtctccacggtgcgaattgcatccaanaattg	2836
QY	1597	ttgatcgaaacccgcaggtgtatctgcgagatgtgtgcgagtgtgtgttggcagatgctgc	1656

Db 2837 colatccaaatgacaaagccatccgcaatctgctggtgagctgcatcccaatgtaatgc 2896
 Qy 1657 gtgagcttcgacgttaagctgacacaaactccgctggaagctggtgttaacaaca 1716
 Db 2897 aagactctgctacagacataatgatacttaacttaacttaacttaacttaactta 2956
 Qy 1717 gttcttgggcaatgltgaagctggtgagatgctggtgaggaacagcaaatgtgta 1776
 Db 2957 aacagttacatttatttaataatgaacaaagcagctggtgattagatgtaactg 3016
 Qy 1777 accatgagaagaatgaaatccgacagatgctggtggtggtggtggtggtggtggt 1836
 Db 3017 atttctgataatgataatgataatgataatgataatgataatgataatgataatg 3076
 Qy 1837 tcaacgacccgaagaagatccgacagctgacgacgacgacgacgacgacgacgac 1896
 Db 3077 ttaagagctcgtgacgaagatgataatgataatgataatgataatgataatgata 3136
 Qy 1897 tactgataatgataatgataatgataatgataatgataatgataatgataatgata 1956
 Db 3137 cgattctgataatgataatgataatgataatgataatgataatgataatgataatg 3196
 Qy 1957 aacaggtcattggtgacgaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1984
 Db 3197 aagagcgctgtgtatgataatgataatgataatgataatgataatgataatgata 3224

RESULT 2

291637/c
 ID 291637 standard; DNA: 260 BP.

AC 291637;

DT 17-MAY-2000 (first entry)

XX E.coli promoter region flanking sequence, DPD3509 lower.

XX Promoter region; regulatory region identification; flanking sequence;

KW cellular insulin; luciferase; thermostable lux gene complex;

KW luxDABE gene complex; crop protection chemical;

XX stress responsive regulatory region; ss.

XX Escherichia coli.

XX US6025131-A.

XX 15-FEB-2000.

XX 23-OCT-1996; 96US-0735545.

XX 23-OCT-1996; 96US-0735545.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Larossa RA, Van Dyk TK;

XX WPI: 2000-181802/16.

XX Example: Column 41-42; 31pp: English.

XX This sequence is a flanking sequence for an E. coli promoter region.

XX The invention relates to a method for identifying regulatory regions

XX modulated by a cellular insulin, comprising: (a) creating a library of

XX gene fusions of genomic DNA fused to a promoterless, luminescent reporter

XX gene complex selected from a gene complex encoding luciferase from

XX Renella species, a thermostable lux gene complex, and a luxCABE gene

XX complex in Enteric bacteria to create fusion-containing strains;

XX (b) culturing individual gene fusion-containing strains in liquid media;

XX (c) contacting the fusion-containing strains at a particular growth

CC phase with a cellular insulin; and (d) analysing the fusion-containing
 CC strain for a change in luminescence, the change in luminescence
 CC indicating that the fusion-containing strain includes a regulatory region
 CC modulated by the cellular insulin. The method is useful for identifying
 CC regulatory regions affected by cellular stress such as that created by
 CC crop protection chemicals. The method can detect promoters or stress
 CC responsive regulatory regions undetectable by prior art methods.
 SX Sequence 260 BP; 53 A; 71 C; 81 G; 55 T; 0 other;

Query Match 4.0%; Score 87.2; DB 21; Length 260;
 Best Local Similarity 58.5%; Pred. No. 6.9e-18;
 Matches 152; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 471 gaagagagcggcgctgtgacggtggtggaatgctgtgactggtggagcgtgcagta 530
 Db 260 GAAGAGAGTGGCGGCTGTGACGGTGTGGAATGCTGTGACTGTTGCACTGCGGTC 201
 Qy 531 tgtctctctctgt 590
 Db 200 TGGCGCGGATCGT 141
 Qy 591 cgaatgt 650
 Db 140 CGCAATACAGT 81
 Qy 651 acgtctctcagaagaacgcacgcacgcacgcacgcacgcacgcacgcacgcacgcac 710
 Db 80 GGCTATTTCAGGAAACCCCAAGAGCTATTTCGCGAATGTACTATTGCGAG 21
 Qy 711 atgtgtatgt 730
 Db 20 CTGCTTTCAGCGCGGAGCA 1

RESULT 3

003827
 ID 003827 standard; DNA: 1713 BP.

AC 003827;

DT 15-FEB-1993 (first entry)

XX Pyruvate oxidase (wild-type).

XX POD; mutation; decarboxylation; assay; ss.

XX Synthetic.

XX DE8333601-A.

XX 05-APR-1990.

XX 03-OCT-1988; 88DE-3833601.

XX 03-OCT-1988; 88DE-3833601.

XX (BOE) BOEHRINGER MANNHEIM GMBH.

XX Mollerling H, Schumacher G;

XX WPI: 1990-108586/15.

XX P-PSDB; R05793.

XX New stable, mutated forms of pyruvate oxidase - having specific

XX aminoacid substitutions, useful as assay reagents, are encoded in

XX Claim 16; Page 6; 10pp; German.

XX The DNA sequence of wild-type POD, given below, may be mutated so

XX that at least 178-Pro and/or 425-Ala of the encoded POD are exchanged.

CC This may be achieved by mutation of nucleotides 532, 533, 534, 1273,
 CC 1274 and/or 1275. Esp. the mutation is of nucleotides 532 and/or 1274
 CC from C to T, resulting in exchange from 178-Pro to Ser and/or 425-Ala
 CC to Val.
 CC The mutated pyruvate oxidase (POD) decarboxylates pyruvate with
 CC formation of H2O2 and is active without addn. of FAD, thiamine
 CC pyrophosphate and divalent metal ions. It is more stable (esp. in
 CC presence of salts and at alkaline pH) than wild-type enzyme, and is
 CC better suited for assay of pyruvate, or pyruvate-generating reactions.
 CC See also 008597.

XX Sequence 1713 BP; 502 A; 315 C; 405 G; 491 T; 0 other;

Query Match 3.4%; Score 72.6; DB 11; Length 1713;
 Best Local Similarity 48.5%; Pred. No. 9.8e-13;
 Matches 235; Conservative 0; Mismatches 244; Indels 6; Gaps 1;

QY 345 gaacaataatgacacttggaaagcgaagtgtaagcgaattatgtgtgtgt 404
 DB 43 gaagcagttatgaagtttagaagcttgaggagatgatttgcgtatcctga 102
 QY 405 gacagccttaacgcatgctgctgcgcacatca-----gatattgagtggtg 458
 DB 103 gttcaataatcaattatgagcgcattatcagcagaagggatcgatccattatatt 162
 QY 459 cagcttcaaatgaagcagcgcttgcagccggtgcggaatcglttgcactgg 518
 DB 163 caagtaagcagtaagaagagttgtgtcaatgagcgctgctgataagtaacgggt 222
 QY 519 gagctggcagatagtgtctcttctgtgctcctgaaacacacacactgattcaaggctct 578
 DB 223 aaatcggggttgccttcgctcagcgagcctgtgtgcacatcattatgatatgtgta 282
 QY 579 tatgattcgcatcgaaatggtgaggaagtglttgccatcgctgacgacattccgggtgc 638
 DB 283 tatgattgctgtgaagacattcccttcttcagcattatgtgtaactact 342
 QY 639 cagattgctcagcttcttcgaagaacgcatcgagatttcttgaagaaatgcctc 698
 DB 343 gggatgaacatgatacgttcccaagaatgaatgaatccgattatgcggagcttga 402
 QY 699 gttactcgcagatgtaatggtgtgagcaggggtgaacgcatatttgcatacgcgatt 758
 DB 403 gattataatgtaacagcgctgaatgtgtcgaagttgcacatgattatgacgaagcaatt 462
 QY 759 cagtcacacatgaggggttaaggtgtgtcgtgtgtaagtattcctcgtgatacgttaag 818
 DB 463 cgacgcgcttaacgcgacccaaggtgtgtgtgtgcaaatccagtcgattaccatg 522
 QY 819 gaaga 823
 DB 523 caaca 527

RESULT 4
 ID 008597
 ID 008597 standard; DNA; 1713 BP.

AC 008597;
 DT 15-FEB-1993 (first entry)

DE Pyruvate oxidase (C532T, C1274T).

KW POD; mutation; decarboxylation; assay; ss.

OS Synthetic.

XX Location/Qualifiers

FT Key mutation 532
 FT /*tag= a
 FT /note= "C -> T; at least one of wild-type C532

FT mutation 1274 and C1274 is exchanged for T"
 FT /*tag= b
 FT /note= "C -> T; at least one of wild-type C532
 FT and C1274 is exchanged for T"

DE3833601-A.

PD 05-APR-1990.

PF 03-OCT-1988; 88DE-3833601.

PR 03-OCT-1988; 88DE-3833601.

PA (BOE) BOEHLINGER MANNHEIM GMBH.

PI Mollering H, Schumacher G;

DR WP1; 1990-108586/15.

DR P-PSDB; R09316.

PT New stable, mutated forms of pyruvate oxidase - having specific
 PT aminoacid substitutions, useful as assay reagents, are encoded in
 PT new DNA

PS Claim 11; Page 6; 10pp; German.

CC The DNA sequence of wild-type POD, given in 008327, may be mutated so
 CC that at least 178-Pro and/or 425-Ala of the encoded POD are exchanged.
 CC This may be achieved by mutation of nucleotides 532, 533, 534, 1273,
 CC 1274 and/or 1275.

CC For example, the sequence given below comprises mutations of
 CC nucleotides 532 and 1274 from C to T, resulting in exchange from
 CC 178-Pro to Ser and 425-Ala to Val.

CC The mutated pyruvate oxidase (POD) decarboxylates pyruvate with
 CC formation of H2O2 and is active without addn. of FAD, thiamine
 CC pyrophosphate and divalent metal ions. It is more stable (esp. in
 CC presence of salts and at alkaline pH) than wild-type enzyme, and is
 CC better suited for assay of pyruvate, or pyruvate-generating reactions.

SO Sequence 1713 BP; 502 A; 313 C; 405 G; 493 T; 0 other;

Query Match 3.4%; Score 72.6; DB 11; Length 1713;
 Best Local Similarity 48.5%; Pred. No. 9.8e-13;
 Matches 235; Conservative 0; Mismatches 244; Indels 6; Gaps 1;

QY 345 gaacaataatgacacttggaaagcgaagtgtaagcgaattatgtgtgtgt 404
 DB 43 gaagcagttatgaagtttagaagcttgaggagatgatttgcgtatcctga 102
 QY 405 gacagccttaacgcatgctgctgcgcacatca-----gatattgagtggtg 458
 DB 103 gttcaataatcaattatgagcgcattatcagcagaagggatcgatccattatatt 162
 QY 459 cagcttcaaatgaagcagcgcttgcagccggtgcggaatcglttgcactgg 518
 DB 163 caagtaagcagtaagaagagttgtgtcaatgagcgctgctgataagtaacgggt 222
 QY 519 gagctggcagatagtgtctcttctgtgctcctgaaacacacacactgattcaaggctct 578
 DB 223 aaatcggggttgccttcgctcagcgagcctgtgtgcacatcattatgatatgtgta 282
 QY 579 tatgattcgcatcgaaatggtgaggaagtglttgccatcgctgacgacattccgggtgc 638
 DB 283 tatgattgctgtgaagacattcccttcttcagcattatgtgtaactact 342
 QY 639 cagattgctcagcttcttcgaagaacgcatcgagatttcttgaagaaatgcctc 698
 DB 343 gggatgaacatgatacgttcccaagaatgaatgaatccgattatgcggagcttga 402
 QY 699 gttactcgcagatgtaatggtgtgagcaggggtgaacgcatatttgcatacgcgatt 758

Db	403	gattataatgtataaacgcgcgtcaatgctgcgaacgcttgccacacatgttatatgacgaagcaatc	462
Oy	759	cagtccaccatcgtcgcggttaaaagctgctgcgttgtagtattccctggtatattcgctaag	818
Db	463	cgacgcgcctcaccgcgcacaaagctgtctgcgttctgtgcaaatccaaatccaaatcgaattacatg	5222
Oy	819	gaaga	823
Db	523	caaca	527
RESULT	5		
ID	T12801	standard; DNA; 2841 BP.	
XX	T12801;		
XX	AC		
XX	08-OCT-1996	(first entry)	
DE	E. coli llycMEDA operon.		
XX	llycMEDA operon; modification; llyG; llyM; llyE; llyD; llyA;		
KW	threonine deaminase; L-valine; L-isoleucine; L-leucine; repression;		
KW	transformation; bacterial host; lipolic acid; H+-ATPase deficient;		
KW	production; high yield; ds.		
XX	Escherichia coli.		
OS			
XX	Key	Location/Qualifiers	
FH	CDS	957..1055	
FT		/*tag- a	
FT	CDS	1195..2841	
FT		/*tag- b	
FT	attenuator	1081..1104	
FT		/*tag- c	
FT	misc_feature	52..57	
FT		/*tag- d	
FT	misc_feature	/note= "SmaI cleavage site"	
FT		2395..2400	
FT		/*tag- e	
FT		/note= "KpnI cleavage site"	
XX			
PN	W09606926-A1.		
PD	07-MAR-1996.		
XX			
XX	30-AUG-1995;	95WO-JP01719.	
XX			
PR	30-AUG-1994;	94JP-0204856.	
XX			
PA	(AJIN) AJINOMOTO CO INC.		
XX			
PI	Hashiguchi K, Ishigooka M, Kurehashi O, Tomita F;		
PI	Yokota A;		
XX			
XX	WPI: 1996-160357/16.		
DR	P-PSDB: W02200, R88842.		
PT	Efficient microbial prodn. of L-valine and L-leucine - by culturing		
PT	Escherichia strain which requires lipolic acid for growth and/or is		
PT	deficient in H+-ATPase		
XX			
XX	Claim 8; Pages 31-36; 53pp; Japanese.		
CC	The present sequence is the E. coli llycMEDA operon, which can be		
CC	modified by the removal of nucleotides 953-1160 to express only		
CC	the llyG, llyM, llyE and llyD genes, but not the llyA (threonine		
CC	deaminase) gene, which is required for L-valine, L-isoleucine		
CC	and/or L-leucine repression. The modified operon can be used to		
CC	transform a bacterial host, esp. E. coli, which requires lipolic		
CC	acid for growth and/or is deficient in H+-ATPase, for the efficient		
CC	prodn. of L-valine and L-leucine in high yield. A specific example		
CC	is the transformed H+-ATPase deficient E. coli strain		

CC	MI45bapDA01/PMWAB6, which when cultured in 1 microg/L lipolic acid
CC	at 37 degrees C for 24 hrs. gave 8.0 g/L L-valine in the medium.
CC	compared to 0.1 g/L for the untransformed strain.
XX	Sequence 2841 BP; 692 A; 707 C; 734 G; 708 T; 0 other;
SO	Query Match 2.8%; Score 60.8; DB 17; Length 2841;
	Best Local Similarity 45.8%; Pred. No. 7.8e-09;
	Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;
QY	341 cgcgaacaacatatttgcaactcttggaagcttgaagagtgtaggaagcgaatttatgcttggc 400
DB	1203 cgcacagctggggtgggtacacgctctgcggcacaagggtctggaacaccgcttctcggtatcc 1262
QY	401 gggtgacagccttaactccgactcgttgatctgtctccgcacatcagatatatggtgtgca 460
DB	1263 ggggtggcgaattatgacgcggtttacgaatgcatctgtatgacgagcgcggtggagcacttgc 1322
QY	461 cgttcgaaatgaggaagcggcgcgcttctgcagccggtgcggaatcgtttgatactgaggga 520
DB	1323 atgcgcacatgagcaggggtgcgcaaatgctgcgtctatcgtttatgtctcgtgtaccggcaa 1382
QY	521 gcttgccagatgtctgcctctcttctgtgtctctgtaaacacacaccctgattcaggctctta 580
DB	1383 aactgcgcgtatctatcgcacacgtctgtctcggcgccaacacccgtatataccgggctttgc 1442
QY	581 tgattccgacatcgaatctgtgctgaaggtgtcttgccatcgtctgaacatattcgcagtgccca 640
DB	1443 ggaagcagctggttagatccatccctcgttctgtctgcatcacgcggtctcaagttccgcacgct 1502
QY	641 gatctgttcgacgctctcttcacggaacacgcacatccggaattctgtcttaaggaaatgctctgg 700
DB	1503 tatcgcaactgacgcaacttccatcagaagtgtatgtctctggatctgtcgttagcctgttaccaa 1562
QY	701 ttactgcgagatcggtggaatggtgtgtgtagcaggggtbaacgcatcttgcataccgcgattca 760
DB	1563 gcatagcttctcgtgtgacgctgcgtggaagattgtccgcgcatcattggtctgaaagcattcga 1622
QY	761 gtccacatcgcggttaagagtgcttctgggtgtagt 796
DB	1623 cgttgcctgctcaggtctgcctgctgcggtcttctgct 1658
RESULT 6	
XX	T07115
XX	T07115 standard; DNA: 2841 BP.
XX	T07115;
XX	15-OCT-1996 (first entry)
DE	E. coli thrABC operon- and ilvGMEDA operon-containing DNA sequence.
XX	thrABC operon; ilvGMEDA operon; thrA gene; ilvA gene; amino acid;
KW	aspartokinase-I; homoserine-dehydrogenase-I; threonine-deaminase;
KM	enzyme; metabolic engineering; L-isoleucine; feedback inhibition; ds.
XX	
OS	Escherichia coli.
XX	
FH	Key Location/Qualifiers
FT	CDS 957..1052
FT	/*tag= a
FT	/label= thrABC operon
FT	CDS 1195..2838
FT	/*tag= b
FT	/label= ilvGMEDA operon
FT	attenuator 1081..1104
FT	/*tag= c
PN	EP685555-A1.
XX	
PD	06-DEC-1995.

XX 30-MAY-1995; 95EP-0108315.
 XX
 XX 30-MAY-1994; 94JP-0116340.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 XX
 XX Hashiguchi K, Kishino H, Matsui H, Tsujimoto N;
 XX WPI: 1996-012380/02.
 XX P-PSDB: R86880, R86881.
 XX
 XX New Escherichia transformant producing L-isoleucine - carrying thr
 XX ABC operon, ilvGMDA operon and Opt. Lys C gene, all of which are
 XX released from feedback inhibition
 XX
 XX Claim 4; Page 35-38; 48pp; English.
 XX
 XX This sequence is present in E. coli and encodes a thrABC operon
 XX which comprises a thrA gene coding for aspartokinase-I-threonine-
 XX dehydrogenase-I which is released from inhibition by L-threonine, and
 XX an ilvGMDA operon which comprises an ilvA gene coding for
 XX threonine-deaminase which is also released from inhibition by L-
 XX isoleucine and which has its region required for attenuation removed.
 XX More specifically, base 953 to 1160 in which resides the attenuator
 XX sequence is deleted. The novel bacterium containing this sequence,
 XX E. coli AJ12919, may be used to produce L-isoleucine.
 XX
 XX Sequence 2841 BP; 692 A; 706 C; 735 G; 708 T; 0 other;

Query Match 2.8%; Score 60.8; DB 17; Length 2841;
 Best Local Similarity 45.8%; Pred. No. 7.8e-09;
 Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;
 XX
 XX 341 cgcgaacaataattgacacttggaaagctcaaggtgtgaagcgaattatgtgtt 400
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 XX Db 1203 cgcgaagtggtgtaactcgttcgagcgaaggtgtgaacacggtttcgtatcc 1262
 XX
 XX 401 ggtgacagccttaacatcgatgtgactgttcgcgcacatcatatgttggtgca 460
 XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 XX Db 1263 ggtggtgcgaattatgcgcggttaccgatgtatgaagcggcggtggacacttgc 1322
 XX
 XX 461 cgttcgaatgaggaagcgcggttgcagccggtgcggaatcgttgcactgggga 520
 XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 XX Db 1323 atgcgacatgagcgaggtgcgcaatgagcggtatcgttgcgtacccggcaa 1382
 XX
 XX 521 gctgcagatggtgtgtcttctgtgtgcctggaaacacacccgtatcagggtctta 580
 XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 XX Db 1383 aactggtatgatacgccacgctgtgcggcggaacacacacgtatgaacccgggtctgc 1442
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 XX 581 tgatcgatcgaaatggtgtcgaaggtgttcgacgcgtacgataccatccagtgccca 640
 XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 XX Db 1443 gagcgcactgttagatccatccctgtgtgttcacatccgcgtacaggtccgaccgt 1502
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 XX 641 gattgttcgaagcttctccaggaacgcaccccgagagatttgtttaaggaatgctctg 700
 XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 XX Db 1503 tatcgccatcgacgacatttcgaaggtgagctgcctggagattcgtttagcctgtaacaa 1562
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 XX 701 ttacgtgaagtggtgaatgtgtgtgagcagggtgaacgacatttggctacgacatca 760
 XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 XX Db 1563 gcatagcttctgtgtgacgtgcgtggaagatltgcgcgcatcalatgcttgacatcga 1622
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 XX 761 gtccacatgagcggtgaaggtgtgtcgtgtgtagt 796
 XX ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 XX Db 1623 cgttgcctgcacaggtgcctcgttcggtcgt 1658

RESULT 7
 ID T62750 standard; DNA; 2841 BP.
 XX
 AC T62750;

XX 14-NOV-1997 (first entry)
 XX
 XX Escherichia coli ilvG gene.
 XX
 XX ilvG; L-isoleucine; production; ds.
 XX
 XX Escherichia coli.
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 XX Key location/Qualifiers
 XX CDS 957..1055
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 XX /product= W13731
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 XX /tag= nf
 XX /product= W13731
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 XX /tag= ng
 XX /product= W1373

QY 581 tgaatcgcacgcgaatggtgcgaagggtgtgcgcacatcgcctgaaccatattccgaatgccca 640
DB 1443 gggagcagcagcttgcattccatccctgtgttcgcacacgcgcaggtgtccgaccgtt 1502
QY 641 gattggttcgacgtcttccagaagaacgcacccgcagatttcttaaggaatgccttg 700
DB 1503 taccgacactgcacgcattccagaagtgatgtccctggagattgcgtttagcctgtacc 1562
QY 701 ttaactgcagatgtgtgaatgtgtgtgacagagggtgaacgcatcttgcatacgcgatcca 760
DB 1563 gataagcttctgtgtgcagtcgctgaagaagtgtccgcgcacatcgtcgaagcattcga 1622
QY 761 gccacacatggcggtgaagggtgtcgtcggtgaagt 796
DB 1623 cgttcgtctcaggtcgtcgtcgttcgttcgttcgt 1658

RESULT 8
Q83259 standard; cDNA: 1928 BP.
AC Q83259;
DT 15-FEB-1996 (first entry)
DE Streptococcus pneumoniae strain pad1 Pad1 cDNA.
XX
XX
KW Pad1: export protein; pox: pox8: virulence determinant;
KW permease like protein; penicillin binding protein; pyruvate oxidase;
KM regulatory element; acellular vaccine; antibody; ds.
XX
OS Streptococcus pneumoniae.
FH
FT Key Location/Qualifiers
FT CDS 154..1927
FT /tag=8
FT /product= pad1
FT
FT
PN WO9506732-A2.
PD 09-MAR-1995.
XX
XX
PF 01-SEP-1994: 94WO-US09942.
XX
XX
PR 01-SEP-1993: 93US-0116541.
PR 18-MAY-1994: 94US-0245511.
XX
XX
PA (UVRQ) UNIV ROCKEFELLER.
XX
XX
PI Measure HR, Pearce BJ, Tuomanen E;
XX
XX
DR WPI: 1995-115448/15.
DR P-PSDB: R87700.
XX
XX
PT Novel gene fragments encoding specific bacterial exported proteins
XX
XX
PS - Specifically of S. pneumoniae, useful as vaccines
XX
XX
XX Claim 11, Page 125-8; 168pp; English.

This sequence represents the cDNA for pad1 (pneumococcal adherence 1). This sequence is also referred to as pox8. Bacteria with mutations in this sequence show an inability to haemagglutinate the GLCNAc6Sial-3gal sugar receptor on neuraminidase-treated bovine erythrocytes. The protein encoded by this sequence shows similarity to enzymes in the acetoxyhydroxy acid synthase-pyruvate oxidase family. This sequence encodes an exported protein of S.pneumoniae. Export proteins are the proteins in pathogenic bacteria that are virulence determinants. This sequence can be inserted into an expression vector (preferably a bacterial expression vector) to provide for high levels of expression of the protein. The protein can then be used in the production of an acellular vaccine. These vaccines are used to provide protection from gram positive bacterial infection. Antibodies against export proteins can be used for diagnosis of infection and in passive immune therapy.

XX SQ Sequence 1928 BP; 596 A; 421 C; 404 G; 507 T; 0 other;
Query Match 2.8%; Score 59.8; DB 16; Length 1928;
Best Local Similarity 46.2%; Pred. No. 1.3e-08;
Matches 236; Conservative 0; Mismatches 272; Indels 3; Gaps 1;
QY 343 cagaacaattatgtacactttggaagctcaaggtgtggaagcgaattatgtttgttg 402
DB 179 ctgcagcaatgcttaacgtatttgaacaacatggtggtgattacattacgtatcccat 238
QY 403 gtgacagccttaatccgatcgtggaatgtgtccgcaaa---taagatatgaatggtg 459
DB 239 caggaacacatcagatcattgatgtgacgcttggctgtgagaacagaatataccgctctac 298
QY 460 acgttcgaatgtggaagcgcgcgttttcacacgcgtgtgcgaatcgtatcacgtggg 519
DB 299 aagltcgcacagaagacagcaggtgtctcttgcaacggttattgcaagctaaatcgcgcgct 358
QY 520 agctgcagatgtgtgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 579
DB 359 caatcggt 418
QY 580 atgattcgcacgcgaatgtgtgcgaagggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 639
DB 419 acgatgcagctatgtgataacatccatccatccatccatccatccatccatccatccatcc 478
QY 640 agattgtgtgcagcttctccagaagaacgcacatccgcgagatttggtaagaatgtctg 699
DB 479 aattgaacatgt 538
QY 700 gttactgcagatgt 759
DB 539 ttatacaacaacgt 598
QY 760 agtccacatgt 819
DB 599 gtgtgtcaattcttaaaaaaggtccacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 658
QY 820 aagacgcaggt 850
DB 659 aagaatacgcagaaactacatactacgtgttc 689

RESULT 9
V52181/C
ID V52181 standard; DNA: 25002 BP.
XX
XX
AC V52181;
XX
XX
DT 23-OCT-1998 (first entry)
XX
XX
DE Streptococcus pneumoniae genome fragment SEQ ID NO:48.
XX
XX
KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
KM computer readable medium; vaccine; pharmaceutical composition; ds.
XX
XX
OS Streptococcus pneumoniae.
XX
XX
PN WO9818931-A2.
XX
XX
PD 07-MAY-1998.
XX
XX
PF 30-OCT-1997: 97WO-US19588.
XX
XX
PR 31-OCT-1996: 96US-0029960.
XX
XX
PA (HUMAN-) HUMAN GENOME SCI INC.
XX
XX
PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
XX
XX
PI Kunsch CA, Rosen CA;
XX

DR 1998-272225/24.

Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumoniae

Claim 1; Page 431-445; 1409pp; English.

The present invention describes a computer readable medium which has on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (VS2134 to VS2524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO: 1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO: 1 to 391, identifying members of the library which contain sequences that hybridize to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.

Sequence 25002 BP; 7422 A; 5498 C; 4618 G; 7463 T; 1 other;

Query Match 2.8%; Score 59.8; DB 19; Length 25002;

Best Local Similarity 46.2%; Pred. No. 6e-08; Matches 236; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

343 cagaacaattatgacacttgaagctcaagtgatgaagcgaattatgtgtgctg 402
DB 6437 CTGCGACATAGCTTAACTATTGAACATGCGGCGTAGATACATCTACGGTATCCAT 6378
403 gtgacagccctaatacgcgtgagatgctgtccgcaaa---tcagatatgaagtgatgc 459
DB 6377 CAGGAACCTCAGCTCATTTGATGACGCTTGGCTGAGACAAAGATATCCGTTCTTAC 6318
460 acgttcgaatgaagaaagcgcggttgcagccggtgagcgaatcgttgatcactggg 519
DB 6317 AAGTTCGCCACGAAAGACAGAGGTGCTTTCGACGCGTTATGCAACGTAATTCGGCGCT 6258
520 agctgcagatagctgtccttctgtgtcgtgaacacacacactgttccagtcctt 579
DB 6257 CAATCGGGGTTGCACTTGTGATGAGTGTCCAGTGCAGTCACTGATTAACGGTGT 6198
580 atgattcgatcgaagaatggtgcaagtggttgcacatcgatgcataatccgagtgccc 639
DB 6197 ACGATGACGATGATGATTAACACTCCATTCCTAGCGATCTTGACATCAGCTTAACG 6138
640 agattggttcgacgtcttcacaggaacgcacatccgagatlltgttaagaatgctctg 699
DB 6137 AATGGAACATGATGCTTTCAGAGGCTTAACCAAAACCAATGTAACAGGTATCGCTG 6078
700 gtactcgtgagatggtgagtggtgagcaggtgtaacgacatttgatcacaagctc 759
DB 6077 TTTACCAACAAACGCTTACTTACGCTGACGATTCGCCAAAGTATTTACGACAGCTGCC 6018
760 agtcacacacagcggtgaagatggtgctgagtgatgcttcctgtgtgataatcgtaag 819
DB 6017 GTGCTGCGAGTTTCTTAAGAAAGTCCAGCTGTTGTAATTCACGTAACCTCGGTTCC 5958
820 aagacgcaggtgagcgttactatccaatc 850
||||| ||||| ||||| ||||| |||||

DB 5957 AAGAAATGATGAAAGAACTCATCTACGAGTTC 5927

RESULT 10

296319/c
ID 296319 standard; DNA: 2280 BP.

XX 296319;

DT 10-APR-2000 (first entry)

DE S. pneumoniae derived DNA from ORF #147.

XX Treatment; prevention; disease; diagnosis; gene therapy; screening;

XX bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss.

XX Streptococcus pneumoniae.

XX OS

XX WO9806734-A1.

XX 19-FEB-1998.

XX 15-AUG-1997; 97WO-US1436.

XX 16-AUG-1996; 96US-0024022.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;

XX Stodola RK;

XX WPI: 1998-159452/14.

XX P-PSDB: Y85970.

XX Streptococcus pneumoniae proteins and related DNA - useful for

XX screening compounds for antibacterial activity

XX Claim 4; Page 180-181; 640pp; English.

This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see 296319-296494) and their encoded proteins (see Y85792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of infection, dysfunction and disease.

Sequence 2280 BP; 639 A; 524 C; 444 G; 673 T; 0 other;

Query Match 2.7%; Score 58.2; DB 19; Length 2280;

Best Local Similarity 46.0%; Pred. No. 4.6e-08; Matches 235; Conservative 0; Mismatches 273; Indels 3; Gaps 1;

343 cagaacaattatgacacttgaagctcaagtgatgaagcgaattatgtgtgctg 402
DB 945 CTGCGACATAGCTTAACTATTGAACATGCGGCGTAGATACATCTACGGTATCCAT 886
403 gtgacagccctaatacgcgtgagatgctgtccgcaaa---tcagatatgaagtgatgc 459
DB 885 CAGGAACCTCAGCTCATTTGATGACGCTTGGCTGAGACAAAGATATCCGTTCTTAC 826
460 acgttcgaatgaagaaagcgcggttgcagccggtgagcgaatcgttgatcactggg 519
DB 825 AAGTTCGCCACGAAAGACAGGTGCTTTCGACGCGTTATGCAACGTAATTCGGCGCT 766
||||| ||||| ||||| ||||| |||||

OY 520 agctggcagatgctgctcttctgtgctcggaaacacacccgattcaggtctt 579
 DB 765 CAATCGGGGTTCAGTTGGTTGAGTGCAGGTCCGACTCATTGATTACGGTGT 706
 OY 580 atgattcgcacatgcaatgctgcaaggtgttgccatcgtcgaatccagtgccc 639
 DB 705 AGGATCGACCTATGATTAACACTCCATTCTTCCATCTTGATACGTCGTTAACG 646
 OY 640 agatttgctcgaagctctcctcaggaacacatccgagatcttcttgaagaaatgctc 639
 DB 645 AATTGACATGATGCTTTCACAAAGACTTACCAAAACCAATGTACAAAGGATGCTG 586
 OY 700 gttactcgcagatgctgtaattgctgctgagcaggtgagacgcatcttcacacgcatc 759
 DB 585 TTACACAAACGTTAGCTTACGCTGAGCAATTGCCAAAGTAATGAGAAAGCTTCC 526
 OY 760 agtccacacacagcgggtgaaggtgctggtgtagtgaatctcgtctgatacgtcaag 819
 DB 525 GTGCTGCACTTTCTTAAAGGCTCCAGCTGTGTGTAATTCAGTAACCTTCGTTCC 466
 OY 820 aagacgcaggtgacggtactatctcgaatcc 850
 DB 465 AAGAAATGATGAAACCTACTACGCTTC 435

RESULT 11
 V55872
 ID V55872 standard; cDNA; 2702 BP.
 AC V55872;

18-NOV-1998 (first entry)

Plant acetolactate synthase (ALS) large subunit protein encoding cDNA.

KW ALS: small subunit; acetolactate synthase: plant; ssuALS; lsuALS;
 KW Nicotiana plumbaginifolia; plasmid vector; herbicide; holoenzyme;
 KW large subunit; ss.

Nicotiana plumbaginifolia.

FH Key Location/Qualifiers
 FT 492..2492
 FT /*tag= a
 FT /product= "ALS large subunit protein"

W09837206-A1.

27-AUG-1998.

23-FEB-1998; 98MO-US03506.

24-FEB-1997; 97US-0039148.

(DUPO) DU PONT DE NEMOURS & CO E I.

Abell LM, Hershey HP;

WPI: 1998-467568/40.

P-PSDH; W79141.

PT New nucleic acid encoding a plant aceto: lactate synthase small
 PT sub:unit - that combines with the large sub:unit to give a
 PT holoenzyme having higher activity than the large sub:unit alone

Example 6; Pages 36-39; 47pp; English.

CC This cDNA encodes the large subunit of a plant acetolactate synthase.
 CC The invention provides a cDNA sequence contained in the plasmid pSSU.NP1
 CC encoding the small subunit of ALS (ssuALS). The plasmid vector comprising
 CC the ssuALS nucleotide operably linked to a regulatory sequence can be
 CC used to transform host cells for the recombinant production of the ssuALS
 CC protein which is used for evaluating a compound for acetolactate synthase

CC inhibition and so for selecting potential herbicides. Evaluation of a
 CC compound for acetolactate synthase (ALS) inhibition comprises expression
 CC and purification of plant ssuALS from the transformed host, mixing this
 CC ssuALS with the large subunit of ALS to form a holoenzyme which is then
 CC treated with a test compound. Treated and untreated holoenzyme activity
 CC are compared to select compounds with potential for herbicidal activity.
 CC Previously, large subunits of plant ALS (lsuALS) have been isolated,
 CC but the existence of ssuALS had not been verified. Mixing the two
 CC subunits results in a holoenzyme that has a 4-15 fold increase in
 CC specific activity over lsuALS alone.

Sequence 2702 BP; 668 A; 645 C; 642 G; 747 T; 0 other;

Query Match 2.6%; Score 56.8; DB 19; Length 2702;
 Best Local Similarity 50.0%; Pred. No. 1.4e-07;
 Matches 170; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

OY 1394 tgtgcctatcacccgaaatgctgctctatcttgaacagctgagataagatgc 1453
 DB 1856 tgaatctatctcctcgcaatgctatccaggtctcagatgagttactaattggaatgc 1915
 OY 1454 ggtgttactggtgataccgagctgcaatgctggtcagatgagttacatcgagaatcc 1513
 DB 1916 tattataagtaactggaatggtgtcaacacagatggtggtccaaataactataagtaacg 1975
 OY 1514 ggaaggaaacgcgactcttggtgtcattccgcacacgagatgctatgctgtgc 1573
 DB 1976 aaag-----ccagcccaatggttgcgtctggtgalttagagagcgtggtatgtgtgc 2032
 OY 1574 tcatgcgattggtgcgaaagtgtgatcgaacccgcaggtgatcgcgattgtgcga 1633
 DB 2033 cgtctgctattggtgcggtcgttgaagaccggatgaaatggtgtgacttgatgagcga 2092
 OY 1634 tgggtgttggtgcaatgctggtggtgagctctgcacggtlaagctgcacacttcgcgt 1693
 DB 2093 tggcagattcatcatgtaattggtcagagctagcaactataagctggaatctccag 2152
 OY 1694 gaagctgtggtgttgaacacagctcttgggcatggtg 1733
 DB 2153 taagattacgttactgataataacacacttgggaatggtg 2192

RESULT 12

N81459

ID N81459 standard; DNA; 2520 BP.

AC N81459;

17-OCT-1990 (first entry)

C3 mutant gene encoding herbicide resistant form of ALS.

Tobacco; acetolactase synthase; sulphonylurea herbicide; ss.

Nicotiana tabacum var. Xanthi.

FH Key Location/Qualifiers
 FT 175..2178
 FT /*tag= a
 FT /label=ALS_gene

EP257993-A.

02-MAR-1988.

20-AUG-1987; 87EP-0307384.

26-AUG-1986; 86US-0900609.

(DUPO) DU PONT DE NEMOURS CO.

Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Yadav NS;

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XX WPI: 1988-058164/09.
DR P-PSDB: P81150.
XX
XX New nucleic acid fragment coding - for mutant aceto-lactate
PT synthetase resistant to sulphonyl-urea herbicides, and
PT transformed resistant crop plants.
XX
XX Disclosure; ; p; English.
XX
XX The sequence encodes a herbicide resistant form of ALS from the C3
CC gene of tobacco. It can be used to improve resistance of eg soya,
CC maize, sugar beet, sunflower, tobacco and potato.
CC See also N81458.
XX
SQ Sequence 2520 BP; 602 A; 564 C; 596 G; 758 T; 0 other;

Query Match          2.6%; Score 55.2; DB 9; Length 2520;
Best Local Similarity 49.7%; Pred. No. 4.5e-07;
Matches 169; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

OY 1394 tgttcctattcaacctgatacgttgcctctatttgaacgagctggcgataagatgc 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1542 tgatgcaattcctccgcaatatgtctatccaggttctagatgagtaactaagtgaatgc 1601

OY 1454 ggtgttactctgtgataccgcaatgtgcaatgtgtgcatgcgaggtacatcgagaatcc 1513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1602 tattataagtaactcgtgtggtgggcaacaccagatgtgggtctcaatactataagtaacag 1661

OY 1514 ggaaggaaacgcgcgaacttctgtgggttcatctccgcacgcgcagatggttaatgcgtgc 1573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1662 aaag---ccacgcgaatgtgtgacatctgtgcgtatgaaggaacaaatggtgttgc 1718

OY 1574 tcatgcaattgtgtgcgaacaaatgtgtgcatcgaacccgagtgatcgcgagtgtgcgca 1633
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1719 cgtcgtctatgtgtgcgtgtgtgtgaagacccgagatgaattgtgtgacattgagtgtga 1778

OY 1634 tgggtgttggcgaatgcgcgtgggtgagctctctgacgttaagctgcaccaactccgct 1693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1779 tggcagtttcatcatgaatgtgcaggaagcttgcacaacttaaggtggagatctccagct 1838

OY 1694 gaagcgtgtgtgttttaacaacagttcttgggcagtgtg 1733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1839 taagattatgtactgaataatacaacacttgggaatgtgt 1878

RESULT 13
Q11495
ID Q11495 standard; DNA; 2520 BP.
XX
XX Q11495;
AC
XX
XX 25-JUL-1991 (first entry)
DT
XX
XX Tobacco SURA-C3 mutant.
DE
XX
XX SURA-C3 mutant; tobacco; acetolactate synthase; ALS; herbicide;
KW resistance; ss.
XX
XX Nicotiana tabacum cv. Xanthi.
OS
XX
XX Key Location/Qualifiers
FH 175..2174
FT CDS /*tag= a
FT /*product= ALS
XX
XX US5013659-A.
XX
XX 07-MAY-1991.
XX
XX 04-MAR-1988; 88US-0164360.
XX

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PR 04-MAR-1988; 88US-0164360.
PR 26-AUG-1986; 86US-0900609.
XX
XX (DUPO ) DU PONT DE NEMOURS CO.
XX
XX Beedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
PI Yadav NS;
XX
XX WPI: 1991-156075/21.
DR P-PSDB: R11974.
XX
XX Nucleic acid fragment - encoding herbicide-resistant plant
PT aceto:lactate synthase protein
XX
XX Disclosure; Fig 5; 65; English.
XX
XX The sequence can confer resistance to chlorsulfuron up to 2 ppb
CC in transformed tobacco calluses.
CC See also Q11495-6.
XX
SQ Sequence 2520 BP; 602 A; 565 C; 594 G; 759 T; 0 other;

Query Match          2.6%; Score 55.2; DB 12; Length 2520;
Best Local Similarity 49.7%; Pred. No. 4.5e-07;
Matches 169; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

OY 1394 tgttcctattcaacctgatacgttgcctctatttgaacgagctggcgataagatgc 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1542 tgatgcaattcctccgcaatatgtctatccaggttctagatgagtaactaagtgaatgc 1601

OY 1454 ggtgttactctgtgataccgcaatgtgcaatgtgtgcatgcgaggtacatcgagaatcc 1513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1602 tattataagtaactcgtgtggtgggcaacaccagatgtgggtctgcatcaactaataagtaacag 1661

OY 1514 ggaaggaaacgcgcgaacttctgtgggttcatctccgcacgcgcagatggtctaatgtcgtgc 1573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1662 aaag---ccacgcgaatgtgtgacatctgtgtgattgaaggaacaaatggtgttgc 1718

OY 1574 tcatgcaattgtgtgcgaacaaatgtgtgcatcgaacccgagtgatcgcgagtgtgcgca 1633
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1719 cgtcgtctatgtgtgcgtgtgtgtgaagacccgagatgaattgtgtgacattgagtgtga 1778

OY 1634 tgggtgttggcgaatgcgcgtgggtgagctctctgacgttaagctgcaccaactccgct 1693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1779 tggcagtttcatcatgaatgtgcaggaagcttgcacaacttaaggtggagatctccagct 1838

OY 1694 gaagcgtgtgtgttttaacaacagttcttgggcagtgtg 1733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1839 taagattatgtactgaataatacaacacttgggaatgtgt 1878

RESULT 14
Q28388
ID Q28388 standard; DNA; 2520 BP.
XX
XX Q28388;
AC
XX
XX 12-FEB-1993 (first entry)
DT
XX
XX Gene from the AUS C3 mutant of tobacco.
DE
XX
XX Herbicide resistant; acetolactate synthase; sulphonylurea;
KW triazopyrimidinesulphonamide; imidazolinone; markers; ss.
XX
XX Nicotiana tabacum.
OS
XX
XX Key Location/Qualifiers
FH 175..2178
FT CDS /*tag= a
FT
XX
XX US5141870-A.
XX

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